



Amendments to the Claims

The following listing of the claims replaces all previous listings.

Please amend claims 1, 3-5, 15, 21, 26, 28, 30, 31, and 33, and cancel claim 45.

1. (currently amended) A method for quantitatively assaying one or more target molecules in a first sample, comprising:
 - (a) adding to the first sample, a preparation of a nucleic acid aptamer specific for ~~each~~ the one or more target molecule;
 - (b) allowing substantially all of the target molecules in the first sample to bind with the aptamer;
 - (c) separating unbound aptamer from the first sample by contacting the sample of step (b) with immobilized ligands, thereby binding the ligands to unbound aptamer, so as to recover a second sample of aptamer bound to target molecules; and
 - (d) using a quantitative replicative procedure comprising a replicative polymerase reaction to determine a quantity of aptamer specific for ~~each~~ the one or more target molecule in the second sample and therefore related to the concentration of target molecule in the first sample.
2. (previously presented) A method according to claim 1, wherein the nucleic acid aptamer is selected from the group consisting of single-stranded DNA, double-stranded DNA, single-stranded RNA, double-stranded RNA and chemical modifications thereof.
3. (currently amended) A method according to claim 1, wherein the one or more target molecule is present in the sample at molar concentrations less than their dissociation constants with respect to the aptamers.
4. (currently amended) A method according to claim 1, wherein the one or more target molecule is present in the sample at molar concentrations

equal to or greater than their dissociation constants with respect to the aptamers.

5. (currently amended) A method according to claim 1, wherein the target ~~molecule~~ molecules are low abundance molecules.
6. (original) A method according to claim 1, where the target molecules include biological macromolecules.
7. (original) A method according to claim 6, wherein the biological macromolecules are selected from the group consisting of a protein, a lipid, a polysaccharide or combinations thereof.
8. (original) A method according to claim 1, wherein the target molecules include small organic molecules.
9. (original) A method according to claim 8, wherein the small organic molecules are selected from a group consisting of antibiotics, vitamins, steroids, and pesticides.
10. (original) A method according to claim 1, wherein the target molecules include inorganic molecules.
11. (original) A method according to claim 10, wherein the inorganic molecules are metal.
12. (original) A method according to claim 11, wherein the metal is selected from a group consisting of metal ions, metal oxides, and metal complexes.
13. (original) A method according to claim 1, wherein the first sample is obtained from an animal subject.

14. (previously presented) A method according to claim 13, wherein the first sample is selected from the group of tissues consisting of organ tissue, muscle tissue, bone tissue, connective tissue, fetal tissue, and placental tissue.
15. (currently amended) A method according to claim 1, wherein the first sample is a biological fluid selected from the group consisting of blood, lymph, urine, sputum, joint fluid, spinal fluid, and saliva.
16. (original) A method according to claim 1, wherein the first sample is an environmental sample.
17. (previously presented) A method according to claim 16, wherein the environmental sample is obtained from a source selected from the group consisting of plants, water, food beverages (including milk), and industrial waste.
18. (previously presented) A method according to claim 1, wherein the immobilized ligand is immobilized on a support matrix selected from the group consisting of resins, beads, magnetic beads, gels, cellulose and silica.
19. (original) A method according to claim 1, wherein the immobilized ligand is immobilized on an affinity column.
20. (original) A method according to claim 1, wherein the quantitative replicative procedure is a quantitative polymerase chain reaction.
21. (currently amended) A method according to claim 1, wherein ~~measuring the amount~~ determining the quantity of aptamer bound to the target

molecule further includes denaturing the aptamer so as to separate the nucleic acid from the target molecules.

22. (original) A method according to claim 21, wherein oligonucleotide primers are added to the sample after denaturing the aptamer from the target molecules.
23. (original) A method according to claim 22, wherein determining the concentration of aptamer includes determining a number of replicative cycles.
24. (original) A method according to claim 6, wherein the target molecules are antibodies.
25. (original) A method according to claim 24, wherein the target molecules include IgE.
26. (currently amended) A method according to claim 1, wherein the one or more target molecules include a plurality of antibody molecules belonging to different subclasses characterized by a difference in the hypervariable region of the antibody.
27. (original) A method according to claim 1, wherein the target molecules are a subclass of an antibody having a characteristic hypervariable region.
28. (previously presented) A method according to any of claims 24-27, wherein the aptamer binds to a constant region of the antibody and wherein the immobilized ligand is the constant region of the antibody for removing unbound aptamer from the sample.

29. (previously presented) A method according to claim 24, wherein the second sample contains antibody-bound aptamer, the second sample being divided into a plurality of aliquots, and a first aliquot of the second sample being assayed using a quantitative replicative procedure to determine an amount of antibody in the first sample.
30. (currently amended) A method according to claim 29, further comprising:
- (a) contacting a second aliquot of the second sample with an immobilized ligand for binding an antibody with a first hypervariable region; wherein the antibody with a first hypervariable region is one of the target molecules in the first sample;
 - (b) recovering a third sample containing the aptamer bound to target molecules excluding the antibody with the first hypervariable region;
 - (c) assaying the aptamer concentration in the third sample using the quantitative replicative procedure, so as to determine a difference in an amount of aptamer in the second sample and the third sample; and
 - (d) obtaining a measure of an amount of the antibody with the first hypervariable region in the first sample from the difference.
31. (currently amended) A method according to claim 29, further comprising:
- (a) contacting a plurality of aliquots of the second sample with an immobilized ligand wherein the ligand is immobilized by attachment to a substrate in a single chamber, or to multiple ligands attached to multiple substrates wherein each substrate is contained in a separate chamber, each immobilized ligand having a specificity for an antibody with a different hypervariable site;
 - (b) recovering a third sample containing the aptamer bound to target molecules excluding the antibody bound to immobilized ligand;

- (c) assaying the aptamer concentration in the third sample using the quantitative replicative procedure, so as to determine a difference in an amount of aptamer in the second sample and the third sample; and
 - (d) obtaining a measure of the antibody with the hypervariable region in the first sample from the difference.
32. (previously presented) A method according to any one of claims 30 or 31, wherein the ligand is a specific antigen.
33. (original) A method according to claim 1, wherein the ligand is a reagent having the aptamer-binding characteristics of the target molecule.
34. (previously presented) A method according to any one of claims 30 or 31, wherein the antibody is IgE.

Claims 35-45. Cancelled.